TTGGGACCCAGCAGGACACAGCAGCAGTCAGGTGCATGCTGGGACCGCGACGGACAGGCTGCCGCACCCCAGGCCCCCA 79

M L A G G V R 7
GAGGCCAGTCTGTTTGCCTCCCAACGCCATCTGACCCAGGTGAGCAAGAGG ATG CTG GCG GGG GGC GTG AGG 151

S M P S P L L A C W Q P I L L L V L G S 27
AGC ATG CCC AGC CCC CTC CTG GCC TGC TGG CAG CCC ATC CTC CTG CTG GTG CTG GGC TCA 211

V L S G S A T G C P P R C E C S A Q D R 47
GTG CTG TCA GGC TCG GCC ACG GGC TGC CCG CCC CGC TGC GAG TGC TCC GCC CAG GAC CGC 271

A V L C H R K R F V A V P E G I P T E T 67
GCT GTG CTG TGC CAC CGC AAG CGC TTT GTG GCA GTC CCC GAG GGC ATC CCC ACC GAG ACG 331

R L L D L G K N R I K T L N Q D E F A S 87
CGC CTG CTG GAC CTA GGC AAG AAC CGC ATC AAA ACG CTC AAC CAG GAC GAG TTC GCC AGC 391

F P H L E E L E L N E N I V S A V E P G 107
TTC CCG CAC CTG GAG GAG CTG GAG CTC AAC GAG AAC ATC GTG AGC GCC GTG GAG CCC GGC 451

A F N N L F N L R T L G L R S N R L K L 127
GCC TTC AAC AAC CTC TTC AAC CTC CGG ACG CTG GGT CTC CGC AGC AAC CGC CTG AAG CTC 511

I P L G V F T G L S N L T K L D T R E N 147
ATC CCG CTA GGC GTC TTC ACT GGC CTC AGC AAC CTG ACC AAG CTG GAC ACG AGG GAG AAC 571

K I V I L L D Y M F Q D L Y N L K S L E 167
AAG ATC GTT ATC CTA CTG GAC TAC ATG TTT CAG GAC CTG TAC AAC CTC AAG TCA CTG GAG 631

V G D N D L V Y I S H R A F S G L N S L 187
GTT GGC GAC AAT GAC CTC GTC TAC ATC TCT CAC CGC GCC TTC AGC GGC CTC AAC AGC CTG 691

E Q L T L E K C N L T S I P T E A L S H 207
GAG CAG CTG ACT CTG GAG AAA TGC AAC CTG ACC TCC ATC CCC ACC GAG GCG CTG TCC CAC 751

L H G L I V L R L R H L N I N A I R D Y 227
CTG CAC GGC CTC ATC GTC CTG AGG CTC CGG CAC CTC AAC ATC AAT GCC ATC CGG GAC TAC 811

S F K R L Y R L K V L E I S H W P Y L D 247
TCC TTC AAG AGG CTG TAC CGA CTC AAG GTC TTG GAG ATC TCC CAC TGG CCC TAC TTG GAC 871

T M T P N C L Y G L N L T S L S I T H C 267
ACC ATG ACA CCC AAC TGC CTC TAC GGC CTC AAC CTG ACG TCC CTG TCC ATC ACA CAC TGC 931

N L T A V P Y L A V R H L V Y L R F L N 287
AAT CTG ACC GCT GTG CCC TAC CTG GCC GTC CGC CAC CTA GTC TAT CTC CGC TTC CTC AAC 991

L S Y N P I S T I E G S M L H E L L R L 307
CTC TCC TAC AAC CCC ATC AGC ACC ATT GAG GGC TCC ATG TTG CAT GAG CTG CTC CGG CTG 1051

Q E I Q L V G G Q L A V V E P Y A F R G 327
CAG GAG ATC CAG CTG GTG GGC GGG CAG CTG GCC GTG GTG GAG CCC TAT GCC TTC CGC GGC 1111

L N Y L R V L N V S G N Q L T T L E E S 347
CTC AAC TAC CTG CGC GTG CTC AAT GTC TCT GGC AAC CAG CTG ACC ACA CTG GAG GAA TCA 1171

FIG. 1 (1 of 2)

```
 V  F  H  S  V  G  N  L  E  T  L  I  L  D  S  N  P  L  A  C   367
GTC TTC CAC TCG GTG GGC AAC CTG GAG ACA CTC ATC CTG GAC TCC AAC CCG CTG GCC TGC  1231

 D  C  R  L  L  W  V  F  R  R  R  W  R  L  N  F  N  R  Q  Q   387
GAC TGT CGG CTC CTG TGG GTG TTC CGG CGC CGC TGG CGG CTC AAC TTC AAC CGG CAG CAG  1291

 P  T  C  A  T  P  E  F  V  Q  G  K  E  F  K  D  F  P  D  V   407
CCC ACG TGC GCC ACG CCC GAG TTT GTC CAG GGC AAG GAG TTC AAG GAC TTC CCT GAT GTG  1351

 L  L  P  N  Y  F  T  C  R  R  A  R  I  R  D  R  K  A  Q  Q   427
CTA CTG CCC AAC TAC TTC ACC TGC CGC CGC GCC CGC ATC CGG GAC CGC AAG GCC CAG CAG  1411

 V  F  V  D  E  G  H  T  V  Q  F  V  C  R  A  D  G  D  P  P   447
GTG TTT GTG GAC GAG GGC CAC ACG GTG CAG TTT GTG TGC CGG GCC GAT GGC GAC CCG CCG  1471

 P  A  I  L  W  L  S  P  R  K  H  L  V  S  A  K  S  N  G  R   467
CCC GCC ATC CTC TGG CTC TCA CCC CGA AAG CAC CTG GTC TCA GCC AAG AGC AAT GGG CGG  1531

 L  T  V  F  P  D  G  T  L  E  V  R  Y  A  Q  V  Q  D  N  G   487
CTC ACA GTC TTC CCT GAT GGC ACG CTG GAG GTG CGC TAC GCC CAG GTA CAG GAC AAC GGC  1591

 T  Y  L  C  I  A  A  N  A  G  G  N  D  S  M  P  A  H  L  H   507
ACG TAC CTG TGC ATC GCG GCC AAC GCG GGC GGC AAC GAC TCC ATG CCC GCC CAC CTG CAT  1651

 V  R  S  Y  S  P  D  W  P  H  Q  P  N  K  T  F  A  F  I  S   527
GTG CGC AGC TAC TCG CCC GAC TGG CCC CAT CAG CCC AAC AAG ACC TTC GCT TTC ATC TCC  1711

 N  Q  P  G  E  G  E  A  N  S  T  R  A  T  V  P  F  P  F  D   547
AAC CAG CCG GGC GAG GGA GAG GCC AAC AGC ACC CGC GCC ACT GTG CCT TTC CCC TTC GAC  1771

 I  K  T  L  I  I  A  T  T  M  G  F  I  S  F  L  G  V  V  L   567
ATC AAG ACC CTC ATC ATC GCC ACC ACC ATG GGC TTC ATC TCT TTC CTG GGC GTC GTC CTC  1831

 F  C  L  V  L  L  F  L  W  S  R  G  K  G  N  T  K  H  N  I   587
TTC TGC CTG GTG CTG CTG TTT CTC TGG AGC CGG GGC AAG GGC AAC ACA AAG CAC AAC ATC  1891

 E  I  E  Y  V  P  R  K  S  D  A  G  I  S  S  A  D  A  P  R   607
GAG ATC GAG TAT GTG CCC CGA AAG TCG GAC GCA GGC ATC AGC TCC GCC GAC GCG CCC CGC  1951

 K  F  N  M  K  M  I  *                                        615
AAG TTC AAC ATG AAG ATG ATA TGA                                1975

GGCCGGGGCGGGGGGCAGGGACCCCCGGGCGGCCGGGCAGGGGAAGGGGCCTGGCCGCCACCTGCTCACTCTCCAGTCC  2054

TTCCCACCTCCTCCCTACCCTTCTACACACGTTCTCTTTCTCCCCTCCCGCCTCCGTCCCCTGCTGCCCCCCCGCCAGCC  2133

CTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCACCTACACAGGGGCATTGACAGAC  2212

TGGAGTTTAAAGCCGACGAACCGACACGCGGCAGAGTCAATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACTTG  2291

GGTTTCAATAATTATGGATTTTTATGAAAACTTGAAATAATAAAAAAAAAAAAAAAAAAG                      2351
```

FIG. 1 (2 of 2)

Input file T81: Output File T811.pat
Sequence length 979

```
                                                                M  A  G  S  P      5
GAATTCGGCACGAGGCCAGCCAGTCCGCCSG/MCGRRGCCCGGCTCGCTGGGGCAGC ATG GCG GGG TCG CCG    72

 L  L  W  G  P  R  A  G  G  V  G  L  L  V  L  L  L  L  G  L   25
CTG CTC TGG GGG CCG CGG GCC GGG GGC GTC GGC CTT TTG GTG CTG CTG CTG CTC GGC CTG  132

 F  R  P  P  P  A  L  C  A  R  P  V  K  E  P  R  G  L  S  A   45
TTT CGG CCG CCC CCC GCG CTC TGC GCG CGG CCG GTA AAG GAG CCC CGC GGC CTA AGC GCA  192

 A  S  P  P  L  A  E  T  G  A  P  R  R  F  R  R  S  V  P  R   65
GCG TCT CCG CCC TTG GCT GAG ACT GGC GCT CCT CGC CGC TTC CGG CGG TCA GTG CCC CGA  252

 G  E  A  A  G  A  V  Q  E  L  A  R  A  L  A  H  L  L  E  A   85
GGT GAG GCG GCG GGG GCG GTG CAG GAG CTG GCG CGG GCG CTG GCG CAT CTG CTG GAG GCC  312

 E  R  Q  E  R  A  R  A  E  A  Q  E  A  E  D  Q  Q  A  R  V  105
GAA CGT CAG GAG CGG GCG CGG GCC GAG GCG CAG GAG GCT GAG GAT CAG CAG GCG CGC GTC  372

 L  A  Q  L  L  R  V  W  G  A  P  R  N  S  D  P  A  L  G  L  125
CTG GCG CAG CTG CTG CGC GTC TGG GGC GCC CCC CGC AAC TCT GAT CCG GCT CTG GGC TTG  432

 D  D  D  P  D  A  P  A  A  Q  L  A  R  A  L  L  R  A  R  L  145
GAC GAC GAC CCC GAC GCG CCT GCA GCG CAG CTC GCT CGC GCT CTG CTC CGC GCC CGC CTT  492

 D  P  A  A  L  A  A  Q  L  V  P  A  P  V  P  A  A  A  L  R  165
GAC CCT GCC GCC CTA GCA GCC CAG CTT GTC CCC GCG CCC GTC CCC GCC GCG GCG CTC CGA  552

 P  R  P  P  V  Y  D  D  G  P  A  G  P  D  A  E  E  A  G  D  185
CCC CGG CCC CCG GTC TAC GAC GAC GGC CCC GCG GGC CCG GAT GCT GAG GAG GCA GGC GAC  612

 E  T  P  D  V  D  P  E  L  L  R  Y  L  L  G  R  I  L  A  G  205
GAG ACA CCC GAC GTG GAC CCC GAG CTG TTG AGG TAC TTG CTG GGA CGG ATT CTT GCG GGA  672

 S  A  D  S  E  G  V  A  A  P  R  R  L  R  R  A  A  D  H  D  225
AGC GCG GAC TCC GAG GGG GTG GCA GCC CCG CGC CGC CTC CGC CGT GCC GCC GAC CAC GAT  732

 V  G  S  E  L  P  P  E  G  V  L  G  A  L  L  R  V  K  R  L  245
GTG GGC TCT GAG CTG CCC CCT GAG GGC GTG CTG GGG GCG CTG CTG CGT GTG AAA CGC CTA  792

 E  T  P  A  P  Q  V  P  A  R  R  L  L  P  P  *                  261
GAG ACC CCG GCG CCC CAG GTG CCT GCA CGC CGC CTC TTG CCA CCC TGA                   840

GCACTGCCCCGGATCCCGTGCACCCTGGGACCCAGAAGTGCCCCCGCCATCCCGCCACCAGGACTGCTCCCCGCCAGCAC  919

GTCCAGAGCAACTTACCCCGGCCAGCCAGCCCTCTCACCCGAGGATCCCTACCCCCTGGC                     979
```

FIG. 2

```
Percent Similarity:                    ty: 29.412

                      .         .         .         .         .
T79          1 MLAGC[illegible]LLACWQPILLLVLGSVLSGS..ATGCPPRCECSAQDR. 47
                    : .:...    || |.:| |::.|: .:|  ..:||. | |. ..:
D45913       1 .....MARLSTGKAAC.QVVLGLLITSLTESSILTSECPQLCVCEIRPWF 44

                      .         .         .         .         .
T79         48 ..........AVLCHRKRFVAVPEGIPTETRLLDLGKNRIKTLNQDEFAS 87
                         .| |:  |:. :|:.:..:|.:| |..|.|
D45913      45 TPQSTYREATTVDCNDLRLTRIPGNLSSDTQVLLLQSNNI.......... 84

                      .         .         .         .         .
T79         88 FPHLEELELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLS 137
                               | ..:.:..|||| .|::. |.:. |. ..:..|.
D45913      85 ...............AKTVDELQQLFNLTELDFSQNNFTNIKEVGLANLT 119

                      .         .         .         .         .
T79        138 NLTKLDTRENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRAFSGLNSL 187
               .||.|.  ||.|  : || :||| ||..| :..|::  || .|||||..|
D45913     120 QLTTLHLEENQISEMTDYCLQDLSNLQELYINHNQISTISANAFSGLKNL 169

                      .         .         .         .         .
T79        188 EQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKV 237
                .| |:. .|. |..  :.  ..| :|.: .   : :| | .|:.| .|:
D45913     170 LRLHLNSNKLKVIDSRWFDSTPNLEILMIGENPVIGILDMNFRPLSNLRS 219

                      .         .         .         .         .
T79        238 LEISHWPYLDTMTPNCLYGLN.LTSLSITHCNLTAVPYLAVRHLVYLRFL 286
               | :.   ||..:..|.| ||: |.|||: . .|. || ||:..:. |:||
D45913     220 LVLAG.MYLTDVPGNALVGLDSLESLSFYDNKLIKVPQLALQKVPNLKFL 268

                      .         .         .         .         .
T79        287 NLSYNPISTIEGSMLHELLRLQEIQLVG.GQLAVVEPY............ 323
               :|. ||| .|::: :.::|||.|:.: . |:|. |:.|
D45913     269 DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELTKLE 318

                      .         .         .         .         .
T79        324 .............AFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLIL 360
                            |||::  |  | :..|.|..: :....|:.|| .: :
D45913     319 ATNNPKLSYIHRLAFRSVPALESLMLNNNALNAVYQKTVESLPNLREISI 368

                      .         .         .         .         .
T79        361 DSNPLACDCRLLWVFRRRWRLNFNRQQPT.CATPEFVQGKEFKDFPDVLL 409
               .|||| ||| : |: ..: .:.|  . .  || |.  .|.:.|   :||:
D45913     369 HSNPLRCDCVIHWINSNKTNIRFMEPLSMFCAMPPEYRGQQVK...EVLI 415

                      .         .         .         .         .
T79        410 PNYFT.CRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKH 458
               .:  . | .   :|  :.:: :| | |: : ||| ::|.|.|.|:.|  :
D45913     416 QDSSEQCLPMISHDTFPNHLNMDIGTTLFLDCRAMAEPEPEIYWVTPIGN 465

                      .         .         .         .         .
T79        459 LVSAKS.NGRLTVFPDGTLEVRYAQVQDNGTYLCIAANAGGNDSMPAHLH 507
                :.... .::..: .:||||:   |::|.| | |:|.|..|.|...| :.
D45913     466 KITVETLSDKYKLSSEGTLEIANIQIEDSGRYTCVAQNVQGADTRVATIK 515

                      .         .         .         .         .
T79        508 V.......................................RSYSPDWPHQ 518
               |                                       :| .. . ..
D45913     516 VNGTLLDGAQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDN 565

                      .         .         .         .         .
T79        519 PNKTF.............................AFISNQPGEGEANSTRA 540
```

FIG. 3 (1 of 2)

```
                |: |:                                    . | .|...: .|
D45913   566 PHITYTARVPVD[illegible]NLTHLQPSTDYEVCLTVSNIHQQTQKSC[illegible]K 615
                    .           .           .           .
T79      541 TVPFPFDIKTLIIATTMGFI..SFLGVVLFCLVLLFLWSRGKGNTKHNIE 588
             |.:|::||..  ..|.:: :  |:::|: :. : ::: .| | .. |:
D45913   616 TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFKRKNYHHSL 665
                    .           .           .           .
T79      589 IEYVPRKSDAGISSADAPRKFNMKMI........................ 614
               .|:.:.|. .:..   |. :|:.
D45913   666 KKYMQKTSSIPLNEL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY 714
```

FIG. 3 (2 of 2)

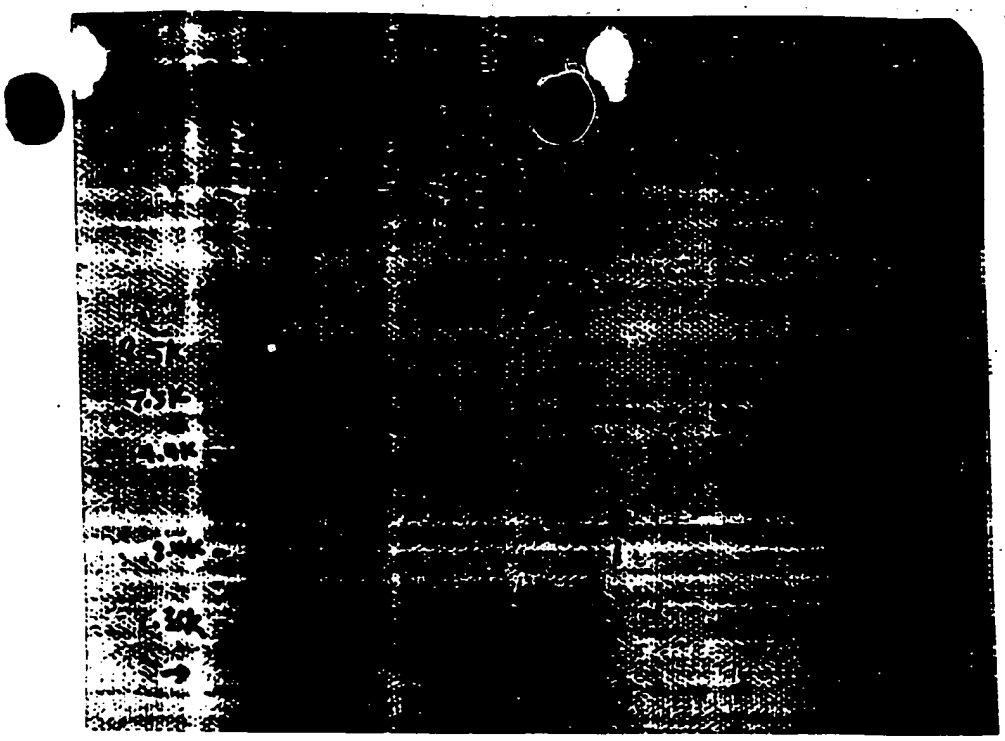

FIG. 4

```
   T   R   P   I   L   V   I   H   D   E   Q   K   G   P   E   V   T   S   N      19
CC ACG CGT CCG ATC TTG GTC ATC CAC GAT GAA CAG AAG GGG CCG GAA GTG ACC TCC AAT    59

 A   A   L   T   L   R   N   F   C   N   W   Q   K   Q   H   N   P   P   S   D    39
GCT GCC CTC ACT CTG CGG AAC TTT TGC AAC TGG CAG AAG CAG CAC AAC CCA CCC AGT GAC  119

 R   D   A   E   H   Y   D   T   A   I   L   F   T   R   Q   D   L   C   G   S    59
CGG GAT GCA GAG CAC TAT GAC ACA GCA ATT CTT TTC ACC AGA CAG GAC TTG TGT GGG TCC  179

 Q   T   C   D   T   L   G   M   A   D   V   G   T   V   C   D   P   S   R   S    79
CAG ACA TGT GAT ACT CTT GGG ATG GCT GAT GTT GGA ACT GTG TGT GAT CCG AGC AGA AGC  239

 C   S   V   I   E   D   D   G   L   Q   A   A   F   T   T   A   H   E   L   G    99
TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA GCC CAT GAA TTA GGC  299

 H   V   F   N   M   P   H   D   D   A   K   Q   C   A   S   L   N   G   V   N   119
CAC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CAG TGT GCC AGC CTT AAT GGT GTG AAC  359

 Q   D   S   H   M   M   A   S   M   L   S   N   L   D   H   S   Q   P   W   S   139
CAG GAT TCC CAC ATG ATG GCG TCA ATG CTT TCC AAC CTG GAC CAC AGC CAG CCT TGG TCT  419

 P   C   S   A   Y   M   I   T   S   F   L   D   N   G   H   G   E   C   L   M   159
CCT TGC AGT GCC TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT GGG GAA TGT TTG ATG  479

 D   K   P   Q   N   P   I   Q   L   P   G   D   L   P   G   T   S   Y   D   A   179
GAC AAG CCT CAG AAT CCC ATA CAG CTC CCA GGC GAT CTC CCT GGC ACC TCG TAC GAT GCC  539

 N   R   Q   C   Q   F   T   F   G   E   D   S   K   H   C   P   D   A   A   S   199
AAC CGG CAG TGC CAG TTT ACA TTT GGG GAG GAC TCC AAA CAC TGC CCT GAT GCA GCC AGC  599

 T   C   S   T   L   W   C   T   G   T   S   G   G   V   L   V   C   Q   T   K   219
ACA TGT AGC ACC TTG TGG TGT ACC GGC ACC TCT GGT GGG GTG CTG GTG TGT CAA ACC AAA  659

 H   F   P   W   A   D   G   T   S   C   G   E   G   K   W   C   I   N   G   K   239
CAC TTC CCG TGG GCG GAT GGC ACC AGC TGT GGA GAA GGG AAA TGG TGT ATC AAC GGC AAG  719

 C   V   N   K   T   D   R   K   H   F   D   T   P   F   H   G   S   W   G   M   259
TGT GTG AAC AAA ACC GAC AGA AAG CAT TTT GAT ACG CCT TTT CAT GGA AGC TGG GGA ATG  779

 W   G   P   W   G   D   C   S   R   T   C   G   G   G   V   Q   Y   T   M   R   279
TGG GGG CCT TGG GGA GAC TGT TCG AGA ACG TGC GGT GGA GGA GTC CAG TAC ACG ATG AGG  839

 E   C   D   N   P   V   P   K   N   G   G   K   Y   C   E   G   K   R   V   R   299
GAA TGT GAC AAC CCA GTC CCA AAG AAT GGA GGG AAG TAC TGT GAA GGC AAA CGA GTG CGC  899

 Y   R   S   C   N   L   E   D   C   P   D   N   N   G   K   T   F   R   E   E   319
TAC AGA TCC TGT AAC CTT GAG GAC TGT CCA GAC AAT AAT GGA AAA ACC TTT AGA GAG GAA  959

 Q   C   E   A   H   N   E   F   S   K   A   S   F   G   S   G   P   A   V   E   339
CAA TGT GAA GCA CAC AAC GAG TTT TCA AAA GCT TCC TTT GGG AGT GGG CCT GCG GTG GAA 1019

 W   I   P   K   Y   A   G   V   S   P   K   D   R   C   K   L   I   C   Q   A   359
TGG ATT CCC AAG TAC GCT GGC GTC TCA CCA AAG GAC AGG TGC AAG CTC ATC TGC CAA GCC 1079

 K   G   I   G   Y   F   F   V   L   Q   P   K   V   V   D   G   T   P   C   S   379
AAA GGC ATT GGC TAC TTC TTC GTT TTG CAG CCC AAG GTT GTA GAT GGT ACT CCA TGT AGC 1139
```

FIG. 5 (1 of 3)

```
 P  D  S  T  S  V  C  V  Q  G  Q  C  V  K  A  G  C  D  R  I   399
CCA GAT TCC ACC TCT GTC TGT GTG CAA GGA CAG TGT GTA AAA GCT GGT TGT GAT CGC ATC  1199

 I  D  S  K  K  K  F  D  K  C  G  V  C  G  G  N  G  S  T  C   419
ATA GAC TCC AAA AAG AAG TTT GAT AAA TGT GGT GTT TGC GGG GGA AAT GGA TCT ACT TGT  1259

 K  K  I  S  G  S  V  T  S  A  K  P  G  Y  H  D  I  I  T  I   439
AAA AAA ATA TCA GGA TCA GTT ACT AGT GCA AAA CCT GGA TAT CAT GAT ATC ATC ACA ATT  1319

 P  T  G  A  T  N  I  E  V  K  Q  R  N  Q  R  G  S  R  N  N   459
CCA ACT GGA GCC ACC AAC ATC GAA GTG AAA CAG CGG AAC CAG AGG GGA TCC AGG AAC AAT  1379

 G  S  F  L  A  I  K  A  A  D  G  T  Y  I  L  N  G  D  Y  T   479
GGC AGC TTT CTT GCC ATC AAA GCT GCT GAT GGC ACA TAT ATT CTT AAT GGT GAC TAC ACT  1439

 L  S  T  L  E  Q  D  I  M  Y  K  G  V  V  L  R  Y  S  G  S   499
TTG TCC ACC TTA GAG CAA GAC ATT ATG TAC AAA GGT GTT GTC TTG AGG TAC AGC GGC TCC  1499

 S  A  A  L  E  R  I  R  S  F  S  P  L  K  E  P  L  T  I  Q   519
TCT GCG GCA TTG GAA AGA ATT CGC AGC TTT AGC CCT CTC AAA GAG CCC TTG ACC ATC CAG  1559

 V  L  T  V  G  N  A  L  R  P  K  I  K  Y  T  Y  F  V  K  K   539
GTT CTT ACT GTG GGC AAT GCC CTT CGA CCT AAA ATT AAA TAC ACC TAC TTC GTA AAG AAG  1619

 K  K  E  S  F  N  A  I  P  T  F  S  A  W  V  I  E  E  W  G   559
AAG AAG GAA TCT TTC AAT GCT ATC CCC ACT TTT TCA GCA TGG GTC ATT GAA GAG TGG GGC  1679

 E  C  S  K  T  C  G  K  G  Y  K  K  R  S  L  K  C  L  S  H   579
GAA TGT TCT AAG ACC TGT GGG AAG GGT TAC AAA AAA AGA AGC TTG AAG TGT CTG TCC CAT  1739

 D  G  G  V  L  S  H  E  S  C  D  P  L  K  K  P  K  H  F  I   599
GAT GGA GGG GTG TTA TCT CAT GAG AGC TGT GAT CCT TTA AAG AAA CCT AAA CAT TTC ATA  1799

 D  F  C  T  M  A  E  C  S  *                                 609
GAC TTT TGC ACA ATG GCA GAA TGC AGT TAA                       1829

GTGGTTTAAGTGGTGTTAGCTCTGAGGGCAAGGCAAAGTGAGGAAGGGCTGGTGCAGGGAAAGCAAGAAGGCTGGAGGG  1908

ATCCAGCGTATCTTGCCAGTAACCAGTGAGGTGTATCAGTAAGGTGGGATTATGGGGGTAGATAGAAAAGGAGTTGAAT  1987

CATCAGAGTAAACTGCCAGTTGCAAATTTGATAGGATAGTTAGTGAGGATTATTAACCTCTGAGCAGTGATATAGCATA  2066

ATAAAGCCCCGGGCATTATTATTATTATTTCTTTTGTTACATCTATTACAAGTTTAGAAAAAACAAAGCAATTGTCAAA  2145

AAAAGTTAGAACTATTACAACCCCTGTTTCCTGGTACTTATCAAATACTTAGTATCATGGGGGTTGGGAAATGAAAAGT  2224

AGGAGAAAAGTGAGATTTTACTAAGACCTGTTTTACTTTACCTCACTAACAATGGGGGGAGAAAGGAGTACAAATAGGA  2303

TCTTTGACCAGCACTGTTTATGGCTGCTATGGTTTCAGAGAATGTTTATACATTATTTCTACCGAGAATTAAAACTTCA  2382

GATTGTTCAACATGAGAGAAAGGCTCAGCAACGTGAAATAACGCAAATGGCTTCCTCTTTCCTTTTTTGGACCATCTCA  2461

GTCTTTATTTGTGTAATTCATTTTGAGGAAAAAACAACTCCATGTATTTATTCAAGTGCATTAAAGTCTACAATGGAAA  2540

AAAAGCAGTGAAGCATTAGATGCTGGTAAAAGCTAGAGGAGACACAATGAGCTTAGTACCTCCAACTTCCTTTCTTTCC  2619

TACCATGTAACCCTGCTTTGGGAATATGGATGTAAAGAAGTAACTTGTGTCTCATGAAAATCAGTACAATCACACAAGG  2698
```

FIG. 5 (2 f 3)

AGGATGAAACGCCGGAACAAAAATGAGGTGTGTAGAACAGGGTCCCACAGGTTTGGGGACATTGAGATCACTTGTCTTG 2777

TGGTGGGGAGGCTGCTGAGGGGTAGCAGGTCCATCTCCAGCAGCTGGTCCAACAGTCGTATCCTGGTGAATGTCTGTTC 2856

AGCTCTTCTGTGAGAATATGATTTTTTCCATATGTATATAGTAAAATATGTTACTATAAATTACATGTACTTTATAAGT 2935

ATTGGTTTGGGTGTTCCTTCCAAGAAGGACTATAGTTAGTAATAAATGCCTATAATAACATATTTATTTTTATACATTT 3014

ATTTCTAATGAAAAAAACTTTTAAATTATATCGCTTTTGTGGAAGTGCATATAAAATAGAGTATTTATACAATATATGT 3093

TACTAGAAATAAAAGAACACTTTTGGAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3147

FIG. 5 (3 f 3)

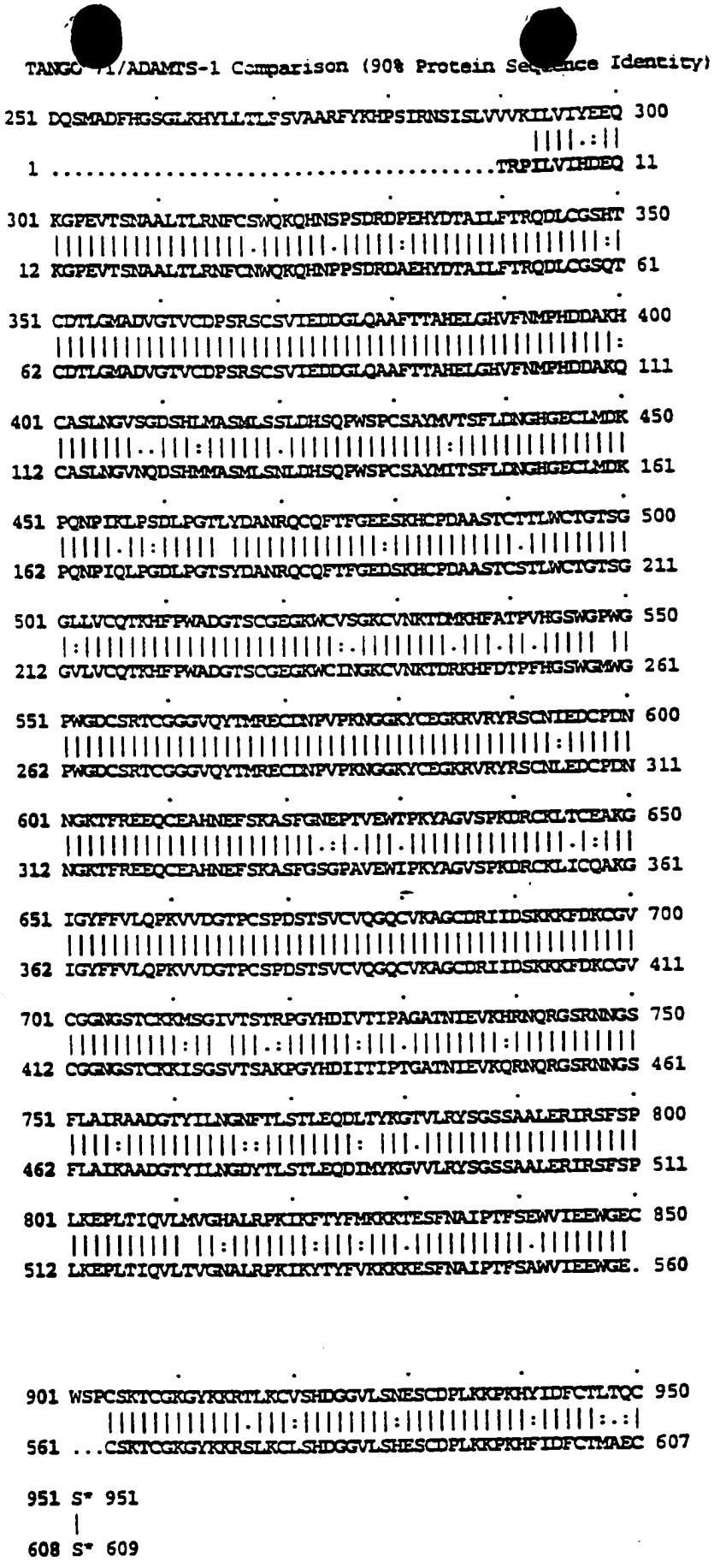
TANGO 71/ADAMTS-1 Comparison (90% Protein Sequence Identity)
251 DQSMADFHGSGLKHYLLTLFSVAARFYKHPSIRNSISLVVVKILVIYEEQ 300
1 .....TRPILVIHDEQ 11
301 KGPEVTSNAALTLRNFCSWQKQHNSPSDRDPEHYDTAILFTRQDLCGSHT 350
12 KGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHYDTAILFTRQDLCGSQT 61
351 CDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKH 400
62 CDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQ 111
401 CASLNGVSGDSHLMASMLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDK 450
112 CASLNGVNQDSHMMASMLSNLDHSQPWSPCSAYMITSFLDNGHGECLMDK 161
451 PQNPIKLPSDLPGTLYDANRQCQFTFGEESKHCPDAASTCTTLWCTGTSG 500
162 PQNPIQLPGDLPGTSYDANRQCQFTFGEDSKHCPDAASTCSTLWCTGTSG 211
501 GLLVCQTKHFPWADGTSCGEGKWCVSGKCVNKTDMKHFATPVHGSWGPWG 550
212 GVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTDRKHFDTPFHGSWGMWG 261
551 PWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNIEDCPDN 600
262 PWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDN 311
601 NGKTFREEQCEAHNEFSKASFGNEPIVEWTPKYAGVSPKDRCKLTCEAKG 650
312 NGKTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKG 361
651 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGV 700
362 IGYFFVLQPKVVDGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGV 411
701 CGGNGSTCKKMSGIVTSTRPGYHDIVTIPAGATNIEVKHRNQRGSRNNGS 750
412 CGGNGSTCKKISGSVTSAKPGYHDIITIPTGATNIEVKQRNQRGSRNNGS 461
751 FLAIRAADGTYILNGNFTLSTLEQDLTYKGTVLRYSGSSAALERIRSFSP 800
462 FLAIKAADGTYILNGDYTLSTLEQDIMYKGVVLRYSGSSAALERIRSFSP 511
801 LKEPLTIQVLMVGHALRPKIKFTYFMKKKTESFNAIPTFSEWVIEEWGEC 850
512 LKEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAWVIEEWGE. 560
901 WSPCSKTCGKGYKKRTLKCVSHDGGVLSNESCDPLKKPKHYIDFCTLTQC 950
561 ...CSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCTMAEC 607
951 S* 951
608 S* 609

FIG. 6

```
gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg  50
         Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu
          1               5                  10

atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt   98
Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly
 15                  20                  25                  30

acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa   146
Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Glu
                 35                  40                  45

tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc   194
Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys
             50                  55                  60

act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct   242
Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro
         65                  70                  75

tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc   290
Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly
     80                  85                  90

aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat   338
Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His
 95                 100                 105                 110

gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt   386
Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys
                115                 120                 125

ggt ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca   434
Gly Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro
            130                 135                 140

aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc   482
Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser
        145                 150                 155

tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag   530
Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu
    160                 165                 170

gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat   578
Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn
175                 180                 185                 190

gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tcg cca aag   626
Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys
                195                 200                 205
```

Fig. 7 (1 of 4)

```
gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc   674
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe
            210                 215                 220

gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct   722
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser
        225                 230                 235

acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc   770
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg
    240                 245                 250

atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga   818
Ile Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly
255                 260                 265                 270

aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga   866
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg
                275                 280                 285

ccc ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att   914
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile
            290                 295                 300

gag gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt   962
Glu Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe
        305                 310                 315

ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc  1010
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe
    320                 325                 330

act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta  1058
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu
335                 340                 345                 350

agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt  1106
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser
                355                 360                 365

cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct  1154
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala
            370                 375                 380

ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aag aca gag  1202
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu
        385                 390                 395

tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg  1250
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp
    400                 405                 410
```

Fig. 7 (2 of 4)

```
ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtg   1298
Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val
415                 420                 425                 430

cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa   1346
Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu
                435                 440                 445

gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac   1394
Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His
            450                 455                 460

tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt   1442
Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly
        465                 470                 475

tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta   1490
Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu
    480                 485                 490

tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac   1538
Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp
495                 500                 505                 510

ttc tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa ggtagcgtgg  1592
Phe Cys Thr Leu Thr Gln Cys Ser
            515

ggaggggctg atacactgag tgcaagagta ctggagggat ccagtgagtc aaaccagtaa 1652
gcagtgaggt gtggcaagga ggtgtgtgta ggggatacat agcaaaggag gtagatcagg 1712
acactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa 1772
gaccatacag agcactaagg agccccaaag cactattagt atctcttttc ttatatctat 1832
cgccccaaata attttcagag tctggcagaa gccctgttgc actgtactaa ctagatactt 1892
ctcatcacaa agattgggaa aggcaaagca gaaagatggt aagactgggt ttcaaacaag 1952
gcttggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc 2012
gctggttgct gtggttttac ggaaggttga tgcatcattc ctatcaacag tgaaaagttc 2072
agcttgttca acgtgacaga aaggctcatc tccgtgaaag agctcctgat ttcttcttac 2132
accatctcag ttcttaacta tagttcatgt tgaggtagaa acaattcatc tatttataaa 2192
atgtacattg gaaaaaaaaa gtgaagttta tgaggtacac ataaaaactg aaggaaacaa 2252
tgagcaacat gcctcctgct ttgcttcctc ctgaggtaaa cctgcctggg gattgaggtt 2312
gtttaagatt atccatggct cacaagaggc agtaaaataa tacatgttgt gccagagtta 2372
gaatggggta tagagatcag ggtcccatga gatggggaac atggtgatca ctcatctcac 2432
atgggaggct gctgcagggt agcaggtcca ctcctggcag ctggtccaac agtcgtatcc 2492
tggtgaatgt ctgttcagct cttctactga gagagaatat gactgtttcc atatgtatat 2552
gtatatagta aaatatgtta ctatgaattg catgtacttt ataagtattg gtgtgtctgt 2612
tccttctaag aaggactata gtttataata aatgcctata ataacatatt tatttttata 2672
catttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732
atagagtatt tatacaatat atgttaacta gaaataataa aagaacactt ttgaatgtgt 2792
atgcctattt tctggagtgg gattaacttc tgggcaagaa atctgatgag acacaaacat 2852
tggacttcaa gacagtttta aattttgggt aaatgaactg tatttcctgt ttatagacgt 2912
actaataaaa aagaagttga tgatgtcttt agtggtaaga ttgttactaa tgtggttggc 2972
aaattgctgt aaagagccag atagtaagca tttatggcat tgtaggctat ctttcctgcc 3032
acaaccatgt gacagtgagt gctttgtagg actgagagca gccataaatg acatgtaaat 3092
```

Fig. 7 (3 of 4)

gataaactgt ggctgtgctt taataaaact ttatttacaa aaaaaaaaa aaa 3145

Fig. 7 (4 of 4)

```
gcggccgctc ccggccggcc caagggacag agccaggctc cgggagcccg caacactcgt 60
cctgagagcc ccggctcctc agcccgctac ggccagggcc tcggcctccg cccccgactc 120
ccgagctcct gccctagagt cgactgggct cccgcccgcg tgggacagac agacggacag 180
ccagccctgc gagggcgcgc ggaccgggcg gaggtgttgt aggaggagac cgaggagggg 240
ggctgggctg gggctggggc cgcgccggca agagagacat gcgattggtg accaagccga 300
gcggacggac agcgcgcccg ag atg cag gtg agc gag agg atg ctg gca ggg  352
                        Met Gln Val Ser Glu Arg Met Leu Ala Gly
                         1               5                  10

ggt atg aga agc atg ccc agc ccc ctc ctg gcc tgc tgg cag ccc atc   400
Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile
                15                  20                  25

ctc ctg ctg gta ctg ggc tca gtg ctg tca ggc tct gct aca ggc tgc   448
Leu Leu Leu Val Leu Gly Ser Val Leu Ser Gly Ser Ala Thr Gly Cys
            30                  35                  40

ccg ccc cgc tgc gag tgc tca gcg cag gac cga gcc gtg ctc tgc cac   496
Pro Pro Arg Cys Glu Cys Ser Ala Gln Asp Arg Ala Val Leu Cys His
        45                  50                  55

cgc aaa cgc ttt gtg gcg gtg ccc gag ggc atc ccc acc gag act cgc   544
Arg Lys Arg Phe Val Ala Val Pro Glu Gly Ile Pro Thr Glu Thr Arg
    60                  65                  70

ctg ctg gac ctg ggc aaa aac cgc atc aag aca ctc aac cag gac gag   592
Leu Leu Asp Leu Gly Lys Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu
75                  80                  85                  90

ttt gcc agc ttc cca cac ctg gag gag cta gaa ctc aat gaa aac atc   640
Phe Ala Ser Phe Pro His Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile
                95                  100                 105

gtg agc gcc gtg gag cca ggc gcc ttc aac aac ctc ttc aac ctg agg   688
Val Ser Ala Val Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg
            110                 115                 120

act ctg ggg ctg cgc agc aac cgc ctg aag ctt atc ccg ctg ggc gtc   736
Thr Leu Gly Leu Arg Ser Asn Arg Leu Lys Leu Ile Pro Leu Gly Val
        125                 130                 135

ttc acc ggc ctc agc aac ttg acc aag ctg gac atc agt gag aac aag   784
Phe Thr Gly Leu Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys
    140                 145                 150

atc gtc atc ctg cta gac tac atg ttc caa gac cta tac aac ctc aag   832
Ile Val Ile Leu Leu Asp Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys
155                 160                 165                 170

tcg ctg gag gtc ggc gac aac gac ctc gtc tac atc tcc cat cga gcc   880
Ser Leu Glu Val Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala
                175                 180                 185
```

Fig. 8 (1 of 2)

```
ttc agc ggc ctc aac agc ctg gaa cag ctg acg ctg gag aaa tgc aat    928
Phe Ser Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn
            190                 195                 200

ctg acc tcc atc ccc acg gag gcg ctc tcc cac ctg cac ggc ctc atc    976
Leu Thr Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile
        205                 210                 215

gtc ctg cgg cta cga cat ctc aac atc aat gcc atc agg gac tac tcc    1024
Val Leu Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser
    220                 225                 230

ttc aag agg ctg tac cga ctt aag gtc tta gag atc tcc cac tgg ccc    1072
Phe Lys Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro
235                 240                 245                 250

tac ctg gac acc ata acc ccc cgg acg cgt ggg tcg ac                 1110
Tyr Leu Asp Thr Ile Thr Pro Arg Thr Arg Gly Ser
                255                 260
```

Fig. 8 (2 of 2)

```
ctcctggatg tgcgcagccg cagagcgctg ctgctgtgcc taatacccat cgctgcgcac 60
ttgacagcca gtccgcccgt ccggagcccg gctcgttggg gcagc atg gcg ggg tcg 117
                                                 Met Ala Gly Ser
                                                  1

ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg   165
Pro Leu Leu Cys Gly Pro Arg Ala Gly Gly Val Gly Ile Leu Val Leu
 5                  10                  15                  20

ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc   213
Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
                25                  30                  35

gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag   261
Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
            40                  45                  50

acg agc act ccc ctc cgc ttg cgt cgg gcc gtg ccc cga gga gag gcg   309
Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
        55                  60                  65

gcg ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag   357
Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
    70                  75                  80

gcc gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat   405
Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
85                  90                  95                  100

cag cag gcg cgt gtc ctg gcg cag ctg ctg cgc gcc tgg ggc tct ccg   453
Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
                105                 110                 115

cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca   501
Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Asp Pro Asp Ala Pro
            120                 125                 130

gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc   549
Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
        135                 140                 145

ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg   597
Pro Gln Cys Met Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
    150                 155                 160

gcg acg aga ctc ctg acg tgg acc ctg agc tgc tgaggtactt gctagggcgg 650
Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
165                 170                 175

atcctcaccg gaagttcgga gccagaggct gctcctgccc cgcgccgcct ccgccgatct 710
gtggaccagg atttgggtcc cgaggtgccc cctgagaacg tactgggggc tctgctacgc 770
gtcaaacgcc tggagaaccc ctcgccccag gcgccggcac gccgcctcct gcctccctga 830
```

Fig. 9 (1 of 2)

```
gcgatgctgc atcctgcacg ccctggaacc caggagcgcc ccagcaaccc tgactccctg 890
ccagcacgtc caaggctgct taccccagca acctcccatc ccctgagccc tcaataaatg 950
ccatctgtag caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1010
aaaaaaaaaa aaaaaaa                                                1027
```

Fig. 9 (2 of 2)